

FIG.1

```

AlaAT1 1:----- 0
AlaAT2 1:----- 0
AlaAT3 1:MRRFLINQAKGLVDHS-RRQ-HHHKSPSFLSPQPRPLASSPPALSRFF--SSTSEMSASD 56
AlaAT4 1:MRRFVIGQAKNLIDQSRRLQLHHHKNLSFVSLIP-PFSAPSDSSSRHLSSSSSDMSASD 59

AlaAT1 1:-MALKALDYDTLNENVKKCQYAVRGE-LYL--R-ASEL--QKEG---KKVIFTNVGNPHA 50
AlaAT2 1:-MSLKALDYESLNENVKNCQYAVRGE-LYL--R-ASEL--QKEG---KKIIFTNVGNPHA 50
AlaAT3 57:STSSLPVTLDSINPKVLKCEYAVRGEIVNIAQKLQEDLKTNKDAYPFDEIIYCNIGNPQS 116
AlaAT4 60:SSSSLPVTLDTINPKVIKCEYAVRGEIVNIAQKLQEDLKTNKDAYPFDEIIYCNIGNPQS 119
          * * * * * * * * * *

AlaAT1 51:LGQKPLTFPRQVVALCQAPFLDDPNV-GM-LFPADAIARAKHYLSLTSG-GLGAYSDSR 107
AlaAT2 51:LGQKPLTFPRQVVALCQAPFLDDPNV-GM-IFPADAIARAKHYLSLTSG-GLGAYSDSR 107
AlaAT3 117:LGQLPIKFFREVLALCDHASLLDESETHGL--FSTDIDRAWRI LDHIPGRATGAYSHSQ 174
AlaAT4 120:LGQQPITFFREVLALCSYALLDESATHGLFRFSSDSIERAWKILDQIPGRATGAYSHSQ 179
          *** * * * * * * * * * *

AlaAT1 108:GLPGVRKEVAEFIQRDGYPSDEPILFLTDGASKGVMQILNCVIRGNGDGILVPVPQYPL 167
AlaAT2 108:GLPGVRKEVAEFIERRDGYPSDEPILFLTDGASKGVMQILNCVIRGQKDGILVPVPQYPL 167
AlaAT3 175:GIKGLRDVIAAGIEARDGFPADPNDFLTDGASPAVHMMQLLSSEKDGILSPIPQYPL 234
AlaAT4 180:GIKGLRDAIADGIEARDGFPADPNDFMTDGASPGVHMMQLITSEKDGILCPIQYPL 239
          * * * * * * * * * *

AlaAT1 168:YSATISLLGGTLVPYYLDESENWGLDVANLRQSVQAARSQGITVRAMVIINPGNPTGQCL 227
AlaAT2 168:YSATISLLGGTLVPYYLESENWGLDVNNLRQSVQAARSQGITVRAMVIINPGNPTGQCL 227
AlaAT3 235:YSASIALHGGSLVPYYLDEATGWGLEISDLKKQLEEARSKGISVRALVVINPGNPTGQVL 294
AlaAT4 240:YSASIALHGGTLVPYYLDEASGWGLEISELKKQLEDARSKGITVRALAVINPGNPTGQVL 299
          *** * * * * * * * * * *

AlaAT1 228:SEANIREILKFCYNEKLVLLGDEVYQQNIYQDERPFISSKKVLMEMGSPFSKEVQLVSFH 287
AlaAT2 228:SEANIREILRFCCDERLVLLGDEVYQQNIYQDERPFISSKKVLMMDGAPISKEVQLISFH 287
AlaAT3 295:AEENQRDIVNFCKQEGVLVLADEVYQENVYVPDKKFHSFKKVARSLGY-GEKDISLVSFQ 353
AlaAT4 300:SEENQRDVVFKCKQEGVLVLADEVYQENVYVPDKKFHSFKKVARSMGY-GEKDLALVSFQ 358
          * * * * * * * * * *

AlaAT1 288:TVSKGYWGECCQRGGYFEMTNLPPRVVEEIIYKVASIALSPNVSAQIFMGLMVNPPKPGDI 347
AlaAT2 288:TVSKGYWGECCQRGGYFEMTNIPRTVEEIIYKVASIALSPNVSAQIFMGLMVSPKPGDI 347
AlaAT3 354:SVSKGYYGECGRGGYMEVTGFTSDVREQIYKMASVNLCSNISGQILASLVMSPKPGDD 413
AlaAT4 359:SVSKGYYGECGRGGYMEVTGFTSDVREQIYKMASVNLCSNISGQILASLIMSPKPGDD 418
          ***** * * * * * * * * * *

AlaAT1 348:SYDQFARESKGILESLRRRARLMTDGFNSCKNVVCNFTEGAMYSFPQIRLPTGALQAAKQ 407
AlaAT2 348:SYDQFVRESKGILESLRRRRARMMDTGFNSCKNVVCNFTEGAMYSFPQIKLPSKAIQAAKQ 407
AlaAT3 414:SYDSYMAERDGISSMAKRAKTLEDALNSLEGVTCNRAEGAMYLFPRLNPQKAI EAAEA 473
AlaAT4 419:SYESYIAEKDGISSLARRAKTLEEALNKLEGVTCNRAEGAMYLFPCLHLPQKAI EAAEA 478
          ** * * * * * * * * * *

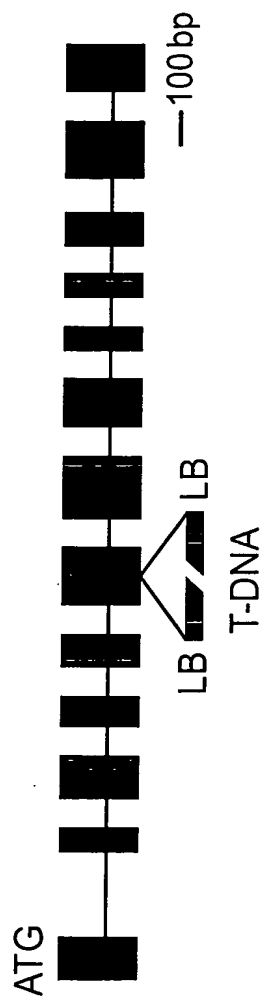
AlaAT1 408:AGKVPDVFYCLKLLEATGISTVPGSGFGQKEGVFHLRTTILPAEDEMPEIMDSFKKFND 467
AlaAT2 408:AGKVPDVFYCLKLLEATGISTVPGSGFGQKEGVFHLRTTILPAEEEMPEIMDSFKKFND 467
AlaAT3 474:EKTAPDAFYCKRLLNATGVVVVPGSGFGQVPGTWHFRCTILPQEDKIPAI VNRLETFHKS 533
AlaAT4 479:EKTAPDNFYCKRLLKATGI VVVVPGSGFRQVPGTWHFRCTILPQEDKIPAI VDRLTA FHQS 538
          ** *** * * * * * * * * * *

AlaAT1 468:FMTQYDNNFGYSKM 481
AlaAT2 468:FMSQYADNFGYSRM 481
AlaAT3 534:FMDEFNRN----- 540
AlaAT4 539:FMDEFNRD----- 545
          **

```

FIG.2

(A)



(B)

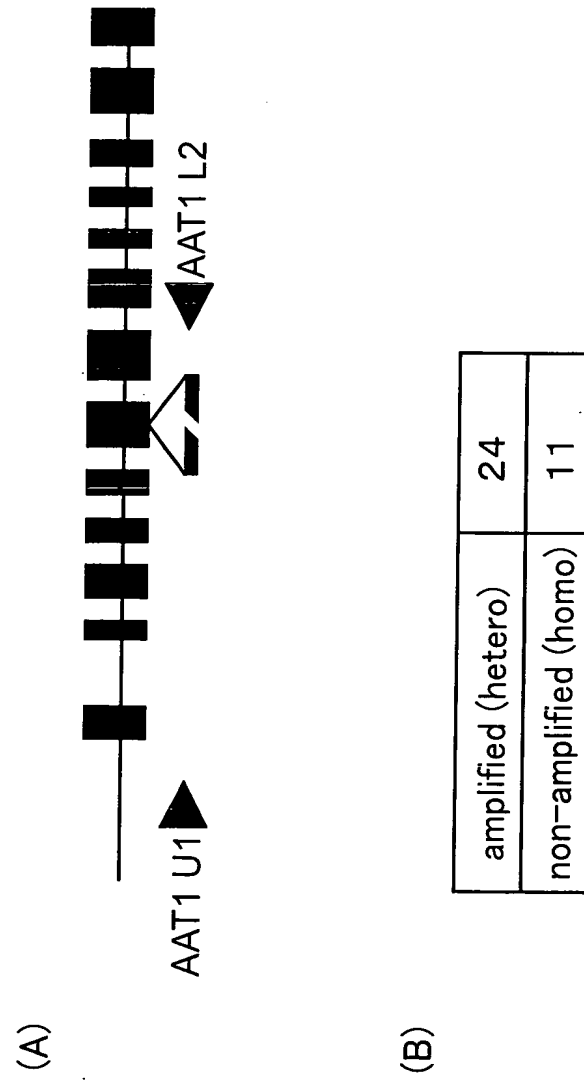
wild

CTG	TTA	GGT	GGT	ACT	CTT	GTT	CCT	TAC	TAT	CTT	GAT	GAG
L	L	G	G	T	L	V	P	Y	Y	L	D	E

8086

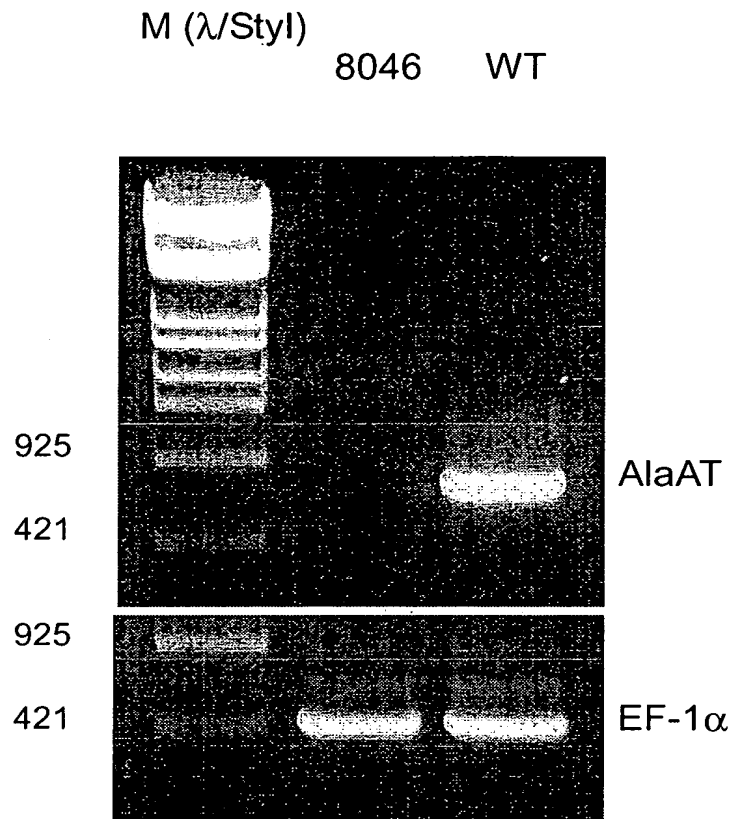
CTG	TTA	GCA	ATT	CAA	TTG	TAA	[T-DNA]	GGTAAT	TAC	TAT	CTT	GAT	GAG
L	L	A	I	Q	L	*							

FIG.3



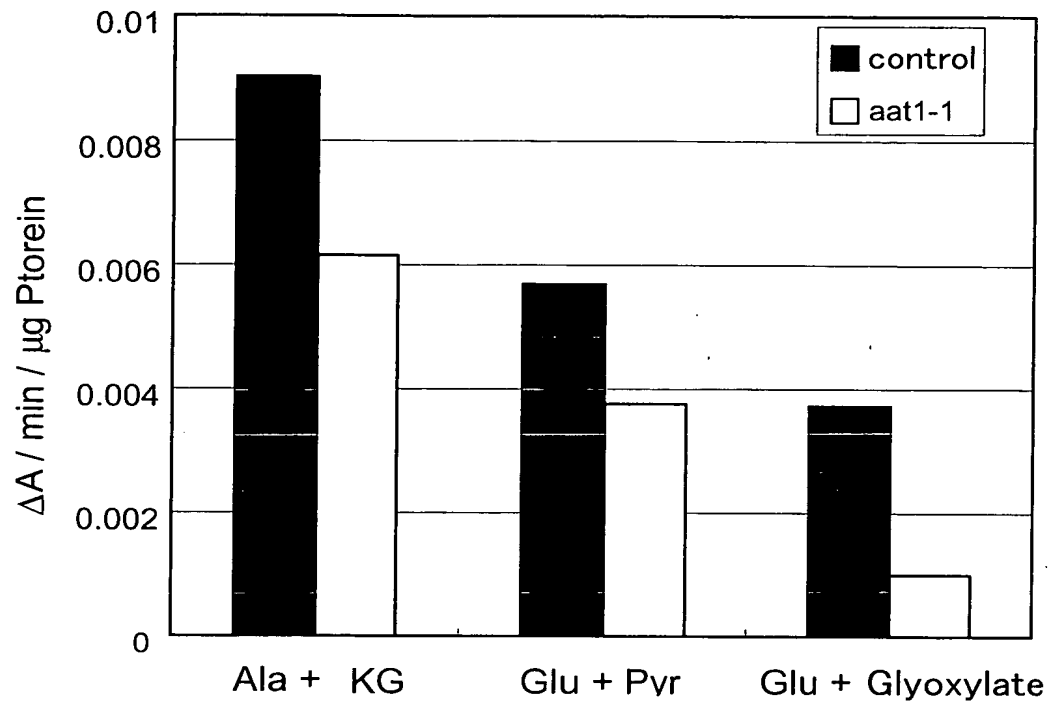
BEST AVAILABLE COPY

FIG.4



BEST AVAILABLE COPY

FIG.5



BEST AVAILABLE COPY

FIG. 6

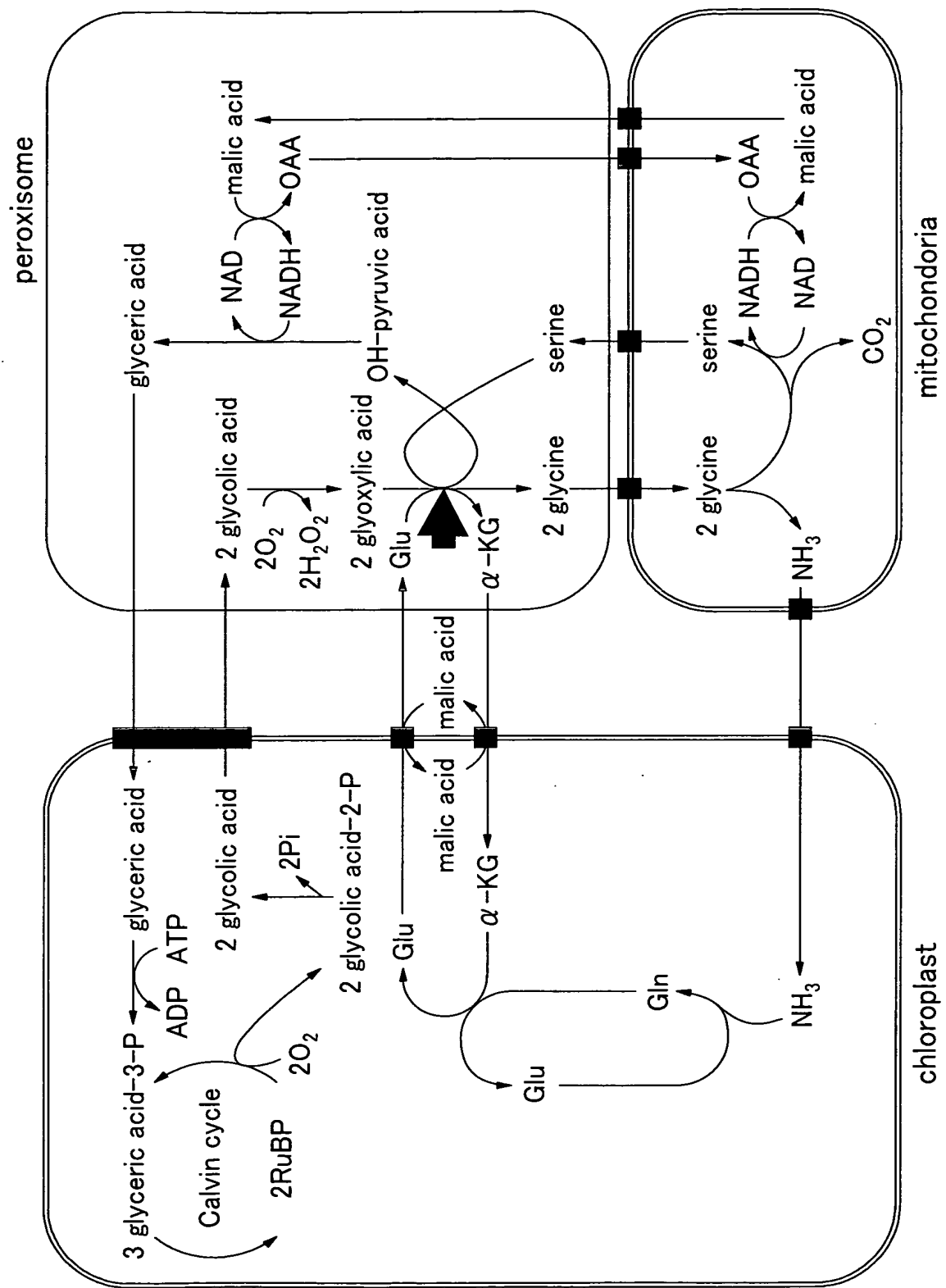


FIG.7

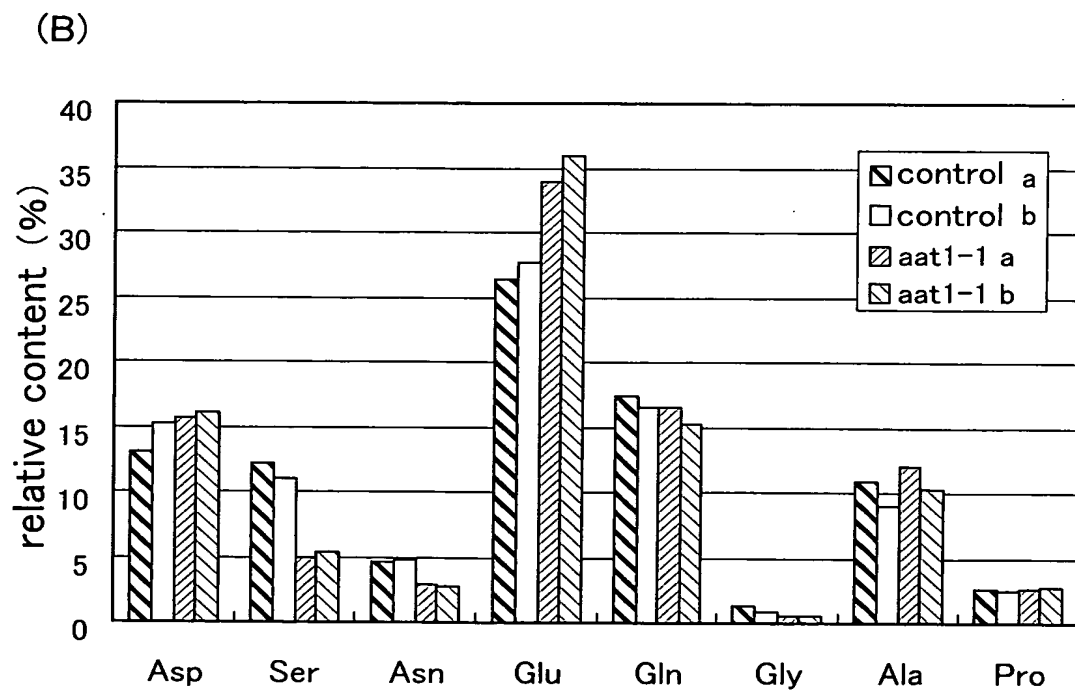
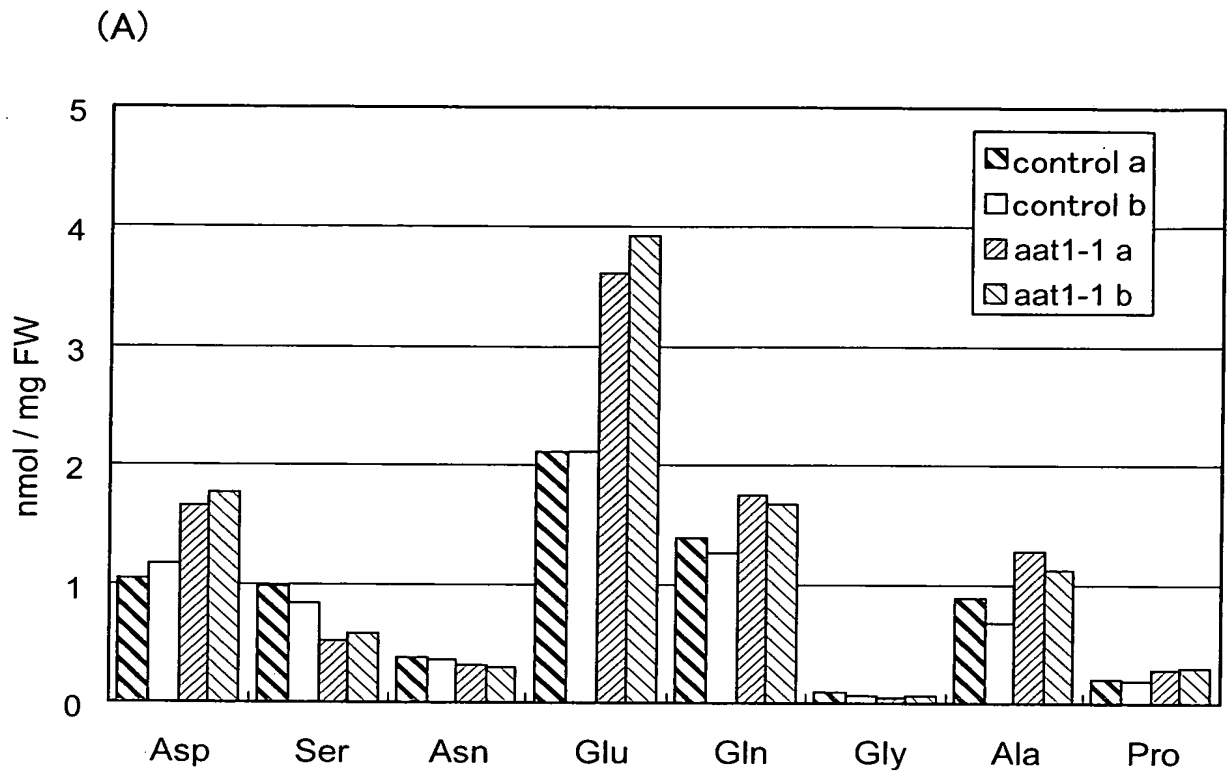


FIG.8

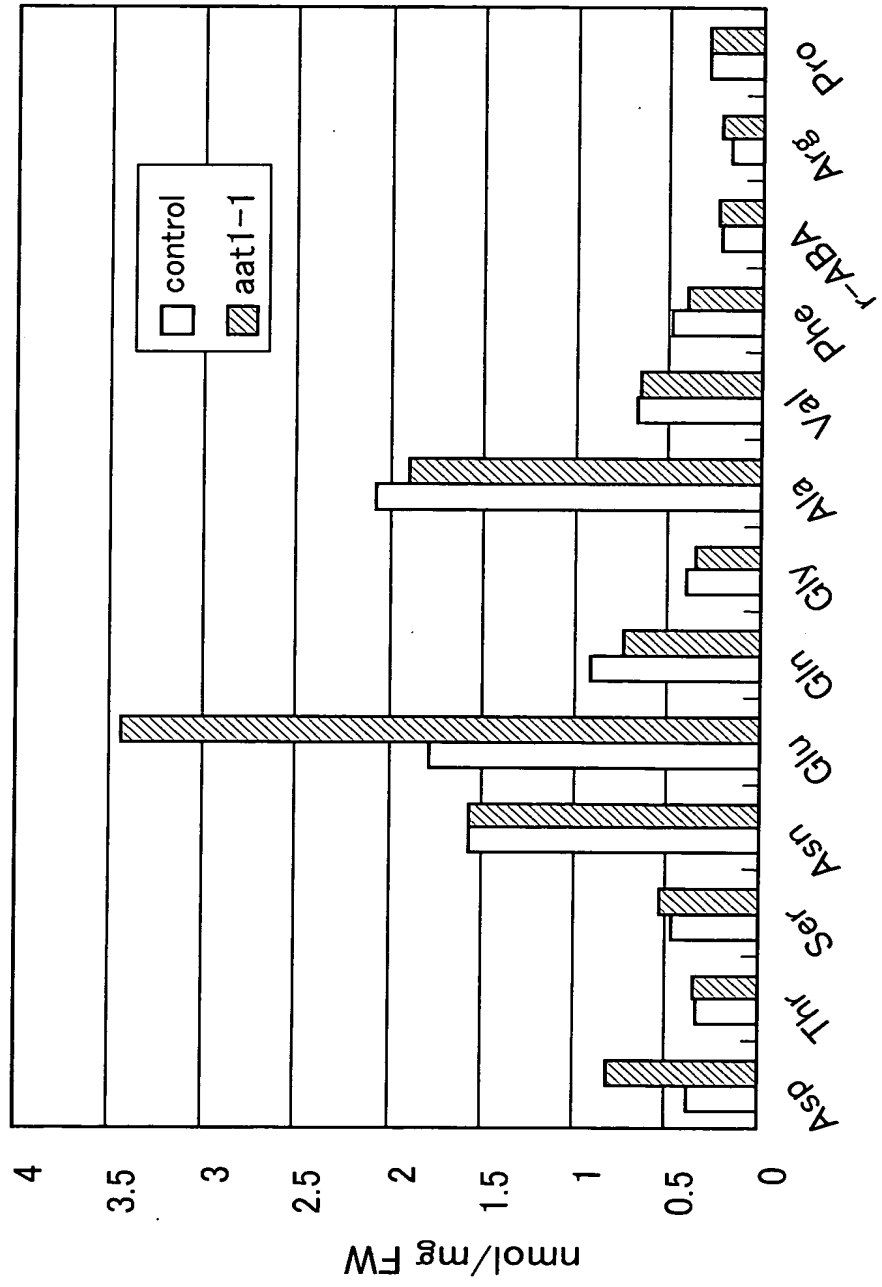


FIG.9

